Abstract

Method for the determination of nucleic and/or amino acid sequences

The present invention relates to a method for the determination of potentially important DNA and/or nucleic acid sequences of a species of interest (species sequences). To provide a method for the determination of DNA and/or nucleic acid sequences in which those DNA and/or nucleic acid sequences which have a potentially increased significance are selected out in a targeted manner, that is to say those which can be investigated in a targeted manner in respect of particular functions, in particular in respect of a potential relevance to disease, with considerably less research expenditure than would be possible with the other DNA sequences which have not been selected in this manner, according to the invention the following steps of the method are proposed:

a) determination of any desired species sequences of the species of interest by biological or genetic engineering methods and storage of the species sequences in a first databank,

b) acquisition of known DNA/nucleic acid sequences of a given group of other species (biosequences), including the functional importance of these sequences, in a second databank in which the biosequences and additional information, including the functional importance of individual biosequences, are stored,

c) comparison of the already known species sequences of the species of interest with the biosequences of the given group of biosequences stored in the second databank in a homology test,

d) separating out of those biosequences of the given group which are homologous to the known species sequences above a given threshold value,

e) comparison of the biosequences from the group mentioned which remain from the second databank and have not been separated out with the species sequences determined according to step a in a second homology test,

h) storage and/or issuing of those species sequences as species sequences of potentially increased importance, homology of which with biosequences from the biosequences remaining from the group mentioned exceeds a given second threshold value, together with information on the biosequences in each case homologous thereto,

i) it being possible optionally also to carry out step e) before step c) and without prior separating out according to step d).

(figure 1)